

**WHAT IS CLAIMED IS:**

1. A trehalose synthase protein with the following amino acid sequence:

Met Ser Ile Pro Asp Asn Thr Tyr Ile Glu Trp Leu Val Ser Gln  
5 10 15

Ser Met Leu His Ala Ala Arg Glu Arg Ser Arg His Tyr Ala Gly  
20 25 30

Gln Ala Arg Leu Trp Gln Arg Pro Try Ala Gln Ala Arg Pro Arg  
35 40 45

10 Asp Ala Ser Ala Ile Ala Ser Val Trp Phe Thr Ala Tyr Pro Ala  
50 55 60

Ala Ile Ile Thr Pro Glu Gly Gly Thr Val Leu Glu Ala Leu Gly  
65 70 75

Asp Asp Arg Leu Trp Ser Ala Leu Ser Glu Leu Gly Val Gln Gly  
15 80 85 90

Ile His Asn Gly Pro Met Lys Arg Ser Gly Gly Leu Arg Gly Arg  
95 100 105

Glu Phe Thr Pro Thr Ile Asp Gly Asn Phe Asp Arg Ile Ser Phe  
110 115 120

20 Asp Ile Asp Pro Ser Leu Gly Thr Glu Glu Gln Met Leu Gln Leu  
125 130 135

Ser Arg Val Ala Ala Ala His Asn Ala Ile Val Ile Asp Asp Ile  
140 145 150

Val Pro Ala His Thr Gly Lys Gly Ala Asp Phe Arg Leu Ala Glu  
25 155 160 165

Met Ala Tyr Gly Asp Tyr Pro Gly Leu Tyr His Met Val Glu Ile  
170 175 180

Arg Glu Glu Asp Trp Glu Leu Leu Pro Glu Val Pro Ala Gly Arg  
185 190 195

30 Asp Ser Val Asn Leu Leu Pro Pro Val Val Asp Arg Leu Lys Glu  
200 205 210

Lys His Tyr Ile Val Gly Gln Leu Gln Arg Val Ile Phe Phe Glu  
215 220 225

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Cont  
B25

Pro Gly Ile Lys Asp Thr Asp Trp Ser Val Thr Gly Glu Val Thr  
 230 235 240

Gly Val Asp Gly Lys Val Arg Arg Trp Val Tyr Leu His Tyr Phe  
 245 250 255

Lys Glu Gly Gln Pro Ser Leu Asn Trp Leu Asp Pro Thr Phe Ala  
 260 265 270

Ala Gln Gln Leu Ile Ile Gly Asp Ala Leu His Ala Ile Asp Val  
 275 280 285

Thr Gly Ala Arg Val Leu Arg Leu Asp Ala Asn Gly Phe Leu Gly  
 290 295 300

Val Glu Arg Arg Ala Glu Gly Thr Ala Trp Ser Glu Gly His Pro  
 305 310 315

Leu Ser Val Thr Gly Asn Gln Leu Leu Ala Gly Ala Ile Arg Lys  
 320 325 330

Ala Gly Gly Phe Ser Phe Gln Glu Leu Asn Leu Thr Ile Asp Asp  
 335 340 345

Ile Ala Ala Met Ser His Gly Gly Ala Asp Leu Ser Tyr Asp Phe  
 350 355 360

Ile Thr Arg Pro Ala Tyr His His Ala Leu Leu Thr Gly Asp Thr  
 365 370 375

Glu Phe Leu Arg Met Met Leu Arg Glu Val His Ala Phe Gly Ile  
 380 385 390

Asp Pro Ala Ser Leu Ile His Ala Leu Gln Asn His Asp Glu Leu  
 395 400 405

Thr Leu Glu Leu Val His Phe Trp Thr Leu His Ala Tyr Asp His  
 410 415 420

Tyr His Tyr Lys Gly Gln Thr Leu Pro Gly Gly His Leu Arg Glu  
 425 430 435

His Ile Arg Glu Glu Met Tyr Glu Arg Leu Thr Gly Glu His Ala  
 440 445 450

Pro Tyr Asn Leu Lys Phe Val Thr Asn Gly Val Ser Cys Thr Thr  
 455 460 465

Ala Ser Val Ile Ala Ala Leu Asn Ile Arg Asp Leu Asp Ala  
 470 475 480  
 Ile Gly Pro Ala Glu Val Glu Gln Ile Gln Arg Leu His Ile Leu  
 485 490 495  
 Leu Val Met Phe Asn Ala Met Gln Pro Gly Val Phe Ala Leu Ser  
 500 505 510  
 Gly Trp Asp Leu Val Gly Ala Leu Pro Leu Ala Pro Glu Gln Val  
 515 520 525  
 Glu His Leu Met Gly Asp Gly Asp Thr Arg Trp Ile Asn Arg Gly  
 530 535 540  
 Gly Tyr Asp Leu Ala Asp Leu Ala Pro Glu Ala Ser Val Ser Ala  
 545 550 555  
 Glu Gly Leu Pro Lys Ala Arg Ser Leu Tyr Gly Ser Leu Ala Glu  
 560 565 570  
 Gln Leu Gln Arg Pro Gly Ser Phe Ala Cys Gln Leu Lys Arg Ile  
 575 580 585  
 Leu Ser Val Arg Gln Ala Tyr Asp Ile Ala Ala Ser Lys Gln Ile  
 590 595 600  
 Leu Ile Pro Asp Val Gln Ala Pro Gly Leu Leu Val Met Val His  
 605 610 615  
 Glu Leu Pro Ala Gly Lys Gly Val Gln Leu Thr Ala Leu Asn Phe  
 620 625 630  
 Ser Ala Glu Pro Val Ser Glu Thr Ile Cys Leu Pro Gly Val Ala  
 635 640 645  
 Pro Gly Pro Val Val Asp Ile Ile His Glu Ser Val Glu Gly Asp  
 650 655 660  
 Leu Thr Asp Asn Cys Glu Leu Gln Ile Asn Leu Asp Pro Tyr Glu  
 665 670 675  
 Gly Leu Ala Leu Arg Val Val Ser Ala Ala Pro Pro Val Ile  
 680 685 690

## 2. A trehalose synthase gene with the following nucleotide sequence:

*Cont  
B2*

	GATCGCTGGC	GTACTGCAGG	TAGAGCAGGC	GCATCGGCC	CCAGGGCGCA	TCGGCCGGCT	60
5	CCGCTGTGCC	CTGCTGGTTC	ATGAAGCGGA	CGAAGCGGCC	ATCGCGGAAC	CGTGGACGCC	120
	ATTGGGGCT	GTCCGGTCG	CGGCTGTCCG	TGAGCGTGCG	CCACAGGTGCG	CTGGAAACG	180
	GCGGACCGCT	CCAAAGCGCG	CCGTGGATGG	GATCGCCGAG	CAGTTCGTGC	AGCTGCCAGG	240
	AACGTTGCCA	ATGCAGCGCG	CCGAGGCTCA	GGCCATGCAG	ATACAGGCCG	GGTCGGCGTT	300
	CGGCCGGCAG	TTCCGGTCCAG	TAGCCATAGA	TCTCGCGAA	TAGCGCGCCG	GCCACGTCGC	360
	GGCCGTAGTC	GGCCTCCACC	AGCAGCGCCA	GCAGGGCTGTT	CAGATAGGAG	TACTGCAACG	420
10	CCACGCTGGC	GATATCGCCG	TGGTGCAGGT	ATTCCACTGC	GTTCATCGCC	GCCGGGTCGA	480
	TCCAGCCGGT	ACCGGTGGGC	GTCACCAGCA	CCAGCACCGA	TGCGCTCGAAG	GCGCCGCTGC	540
	GCTGCAGCTC	GCGCAAGGCC	AGACGCC	GCTGGCCGGG	GGTCTCTGCC	GCGCGCAGAC	600
	CGACGTAGAC	GCGAATCGGC	TCGAGCGCCG	AGCGGCGCT	CAAGACGCTG	ATATCCGCCG	660
	CCGACGGGCC	GGAGGCCATG	AACTCGCGGC	CGGPGCGGCC	CAGCTCCCTCC	CAGCGCAGCA	720
	ACGAGGCCCG	GCTGCCGCTT	TTCAGCGCCG	AGGCCGGTGG	CGCCGTCTCC	GGTCGATCA	780
15	GGGCGTCGTA	CTGCGCGAAG	GATCGTCCA	GCATGCGCAG	TGCCCGCGCC	GCCAGCACAT	840
	CGCTGAGCAG	CGACCAGAAC	AGCGCCAGCG	CCACCAGCAC	GCCGATCACG	TTGGCCAGGC	900
	GCCGTGGCAG	CACCGGGTCG	GGTCCCGCG	AGACGAAGCG	CGACACCAGC	CGATACAGAC	960
	GCGCCAGCGT	CAGCAGGATG	AGAAAGGTGCG	CCAGCGCGGT	GAGAATGACT	TCGAGCAGGT	1020
	GCGCACTGCT	CACCGGGCGGC	ATGCCCATCA	GCGCGCGTAC	CGCGTTCTGC	CAGCCGGCGA	1080
20	CCTGGCTGAG	GAAATACCGG	GCCAGCAGCA	GGCAGCCGAC	CGCGATCAGC	AGATTGACCC	1140
	GCTCGCGCTG	CCAGCGTGGG	CGCTCCGGCA	GTTCCAGATA	GCGCCACAGC	CAGCGCCAGA	1200
	ACACGCCGAG	GCCATAGCCC	ACCGCCAGCG	CCGCGCCGGC	CAGCACGCC	TGGCTCAGCG	1260
	TCGAGCGCCG	CAGCAGCGAT	GGCGTCAGCG	CCGCGCAGAA	GAACAGCGTG	CCCAGCAGCA	1320
	GGCCGAAACC	GGACAGCGAG	CGCCAGATAT	AGAGGACGGG	CAGGTGCAGC	ATGAAGATCT	1380
25	CCGCGGTCCG	GTGACGGCGT	CGCGCCTCGG	CATATCGAGG	CGTGTCCGGT	CGTGCGGTTC	1440
	CCGTGATGGT	CCGCAGCAGG	CCAATCCGAT	GCAACGATGG	CCGAGCGGCC	GACTCAAACG	1500
	TCTACATTT	CCTAGTGCTG	CCGGAACCGA	TCGCCG			1536
	ATG AGC ATC CCA GAC AAC ACC TAT ATC GAA TGG CTG GTC AGC CAG TCC						1584
	ATG CTG CAT GCG GCC CGC GAG CGG TCG CGT CAT TAC GCC GGC CAG GCG						1632
30	CGT CTC TGG CAG CGG CCT TAT GCC CAG GCC CGC CCG CGC GAT GCC AGC						1680
	GCC ATC GCC TCG GTG TGG TTC ACC GCC TAT CCG GCG GCC ATC ATC ACG						1728
	CCG GAA GGC GGC ACG GTA CTC GAG GCC CTC GGC GAC GAC CGC CTC TGG						1776
	AGT GCG CTC TCC GAA CTC GGC GTG CAG GGC ATC CAC AAC GGG CCG ATG						1824

	AAG CGT TCC GGT GGC CTG CGC GGA CGC GAG TTC ACC CCG ACC ATC GAC	1872
	GGC AAC TTC GAC CGC ATC AGC TTC GAT ATC GAC CCG AGC CTG GGG ACC	1920
	GAG GAG CAG ATG CTG CAG CTC AGC CGG GTG GCC GCG GCG CAC AAC GCC	1968
	ATC GTC ATC GAC GAC ATC GTG CCG GCA CAC ACC GGC AAG GGT GCC GAC	2016
	TTC CGC CTC GCG GAA ATG GCC TAT GGC GAC TAC CCC GGG CTG TAC CAC	2064
	ATG GTG GAA ATC CGC GAG GAG GAC TGG GAG CTG CTG CCC GAG GTG CCG	2112
	GCC GGG CGT GAT TCG GTC AAC CTG CTG CCG GTG GTC GAC CGG CTC	2160
	AAG GAA AAG CAC TAC ATC GTC GGC CAG CTG CAG CGG GTG ATC TTC TTC	2208
	GAG CCG GGC ATC AAG GAC ACC GAC TGG AGC GTC ACC GGC GAG GTC ACC	2256
10	GGG GTC GAC GGC AAG GTG CGT CGC TGG GTC TAT CTG CAC TAC TTC AAG	2304
	GAG GGC CAG CCG TCG CTG AAC TGG CTC GAC CCG ACC TTC GCC GCG CAG	2352
	CAG CTG ATC ATC GGC GAT GCG CTG CAC GCC ATC GAC GTC ACC GGC GCC	2400
	CGG GTG CTG CGC CTG GAC GCC AAC GGC TTC CTC GGC GTG GAA CGG CGC	2448
	GCC GAG GGC ACG GCC TGG TCG GAG GGC CAC CCG CTG TCC GTC ACC GGC	2496
15	AAC CAG CTG CTC GCC GGG GCG ATC CGC AAG GCC GGC GGC TTC AGC TTC	2544
	CAG GAG CTG AAC CTG ACC ATC GAT GAC ATC GCC GCC ATG TCC CAC GGC	2592
	GGG GCC GAT CTG TCC TAC GAC TTC ATC ACC CGC CCG GCC TAT CAC CAT	2640
	GCG TTG CTC ACC GGC GAT ACC GAA TTC CTG CGC ATG ATG CTG CGC GAA	2688
	GTG CAC GCC TTC GGC ATC GAC CCG GCG TCA CTG ATC CAT GCG CTG CAG	2736
20	AAC CAT GAC GAG TTG ACC CTG GAG CTG GTG CAC TTC TGG ACG CTG CAC	2784
	GCC TAC GAC CAT TAC CAC TAC AAG GGC CAG ACC CTG CCC GGC GGC CAC	2832
	CTG CGC GAA CAT ATC CGC GAG GAA ATG TAC GAG CGG CTG ACC GGC GAA	2880
	CAC GCG CCG TAC AAC CTC AAG TTC GTC ACC AAC GGG GTG TCC TGC ACC	2928
	ACC GCC AGC GTG ATC GCC GCG CTT AAC ATC CGT GAT CTG GAC GCC	2976
25	ATC GGC CCG GCC GAG GTG GAG CAG ATC CAG CGT CTG CAT ATC CTG CTG	3024
	GTG ATG TTC AAT GCC ATG CAG CCC GGC GTG TTC GCC CTC TCC GGC TGG	3072
	GAT CTG GTC GGC GCC CTG CCG CTG GCG CCC GAG CAG GTC GAG CAC CTG	3120
	ATG GGC GAT GGC GAT ACC CGC TGG ATC AAT CGC GGC GGC TAT GAC CTC	3168
	GCC GAT CTG GCG CCG GAG GCG TCG GTC TCC GCC GAA GGC CTG CCC AAG	3216
30	GCC CGC TCG CTG TAC GGC AGC CTG GCC GAG CAG CTG CAG CGG CCA GGC	3264
	TCC TTC GCC TGC CAG CTC AAG CGC ATC CTC AGC GTG CGC CAG GCC TAC	3312
	GAC ATC GCT GCC AGC AAG CAG ATC CTG ATT CCG GAT GTG CAG GCG CCG	3360
	GGA CTC CTG GTG ATG GTC CAC GAG CTG CCT GCC GGC AAG GGC GTG CAG	3408

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4150

4210

4270

4330

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CTC ACG GCA CTG AAC TTC AGC GCC GAG CCG GTC AGC GAG ACC ATC TGC  
 5 CTG CCC GGC GTG GCG CCC GGC CCG GTG GTG GAC ATC ATT CAC GAG AGT  
 GTG GAG GGC GAC CTC ACC GAC AAC TGC GAG CTG CAG ATC AAC CTC GAC  
 CCG TAC GAG GGG CTT GCC CTG CGT GTG AGC GCC GCG CCG CCG GTG  
 ATC TGA GCGC  
 CCTCTTCGGCG CGCCCCGGGT CGCCCGCTAT AGTGCAGCAGC GCCTGGGGCG CGCATTGCC  
 10 TCGCCGTCGA GACCAGCCCG TGTCGTTCAC TTGCGTTTTC CGCCTTGCCT TGCTGCCGCT  
 GGCGCTGCTT GCCGCACCCG TCTGGGCGCA GACCGCCTGC CCGCCCGGCC AGCAGCCGAT  
 CTGCCCTGAGC GGCAGCTGCC TCTGCGTGCC GGCCGCCGCC AGCGATCCAC AGGCGGTCTA  
 15 CGACCGCGTG CAGCGTATGG CTACGCTGGC CCTGCAGAAC TGGATCCAGC AGTCGCGCGA  
 CCGCCTGATG GCCGGCGCG TCGAGCCGAT ACCGCTGCAC ATCCGCTCGC AGCTCGAGCC  
 GTATTCGAT CTTGCCGTGC TGGAGAGTGC GCGGTACCGC GTCGCGACG AGGTGGTGCT  
 GACTGCCGGC AACACCCCTGC TGCACAACCC GGACGTCAAT GCCGTGACCC TGATCGACGT  
 CATCGTCTTC CGCCACGAGG AGGATGCCCG GGACAACGTC GCGCTCTGGG CCCATGAGCT  
 20 CAAGCACGTC GAGCAATATC TGGACTGGGG CGTCGCCAG TTGCGCCGCC GCTATACGCA  
 GGATTTCCGT GCCGTGGAGC GCCCGGCCATA TGCCTGGAG CGTGAGGTGG AAGAGGCCCT  
 GCGCGAGACG CAGACCGCGC GCTGAGCGAG CTGATCGGTG CTGCTGCCCG CACTGGGCTG  
 AAGCCCACCA ATGACGCCGG CGAAAACGAA AAACCCGCC GAGGCGGGGT TTCTGACGCG  
 GGTTGTGCCG TCAGCTCAGA ACCCCGGGAC CACGGCCGCC TTGTACTTT CCTCGATGAA  
 25 CTGGCGTACT TGCTCCCTGT GCAGCGCGGC AGCCAGTTTC TGATGGCAT CGCTGTCC  
 GTTGTCCCGA CGGGCGACCA GAATGTTCAC GTATGGCGAG TCGCTGCCCT CGATCACCAG  
 GGCCTCCTGG GTCGGGTTCA GCTTGGCTTC CAGCGCGTAG TTGGTGTGA TCAGCGCCAG  
 GTCGACCTGG GTCAGCACGC GCGGCAGAGT CGCGGCTTCC AGTCGCGGA TCTTGATCTT  
 CTTCGGGTTTC TCGGCCATGT CTTCGGCGTG GCGGTGATGC CGGGCGCCGTC CTTCAGACCG  
 ATC  
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3. A recombinant plasmid containing the trehalose synthase gene of claim 1.

4. The recombinant plasmid according to claim 1 which is recombinant plasmid  
 pCJ122.

5. A transformed *E. coli* with the recombinant plasmid of claim 1.

6. The transformant according to claim 5 in which the recombinant plasmid is pCJ122.

7. A process for producing trehalose which comprises reacting the trehalose synthase enzyme of claim 1 with maltose solution to obtain trehalose.

*Cont  
B2* 5 8. A process for producing trehalose which comprises crushing the transformed *E. coli* of claim 5, centrifuging the crushed bacteria, and reacting the resulting supernatant with maltose solution to obtain trehalose.

10 9. A novel microorganism *Pseudomonas stutzeri* CJ38 that produces trehalose from maltose.

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